Whole Genome Sequencing of Toxin Genes in *S. aureus* isolates from healthy individuals

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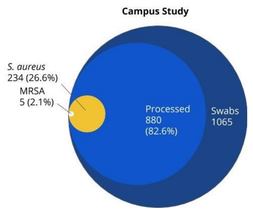
Background:

- *Staphylococcus aureus* is a commensal and opportunistic bacteria found in nasal cavities of ~30% of the population
- The study has collected nasal swabs from healthy individuals on Concordia St. Paul Campus (CSP) and are tested to determine if they are *S. aureus*



Methods:

- 142 isolates were sent to the Minnesota Department of Health infectious disease lab to be whole genome sequenced
- Isolates were analyzed to determine toxin prevalences
- Isolates were further analyzed to check for Mobile Genetic Elements (MGEs)
  - None = Isolate was absent of all toxin genes
  - All = Isolate contained presence of all toxin genes
  - Mix = Isolate was absent of a toxin gene/s but contained the other toxin gene/s

Discussion:

- Part A: Toxin Prevalences
  - Out of 142 isolates, the superantigens were present in:
    - SEH (3), SEIX (113), SEC (4), SEIL (4), TSST-1 (16), SEB (17), SEIK (17), SEIQ (15), SED (3), SEJ (4), SEIR (4), SEIP (13), SEA (24), SEG (61), SEI (64), SEIM (66), SEIN (56), SEIO (64), SEIU+ (61), and SEIV (9)
- Part B: Mobile Genetic Element (MGE) Prevalences
  - Out of 142 isolates, the MGEs were present in:
    - SaPIbov (0), SaPI3 (13), pIB485 (3), IEC (0), Sa3 (17), EGC 1 (48), EGC 2/3 (47) and EGC 4 (6)
- Part A and B:
  - The prevalence of EGC 1(48) and 2/3 (47) is similar to the prevalence of the SAgs found in the EGCs (56-66)
    - The lack of EGC 4 could contribute to the low prevalence of SEIV
  - pIB485 (3) and SaPI3 (13) prevalences are similar to the prevalences of the SAgs they contain (3-4) and (15-17)
  - Lack of SaPIbov and IEC suggest those toxins came from other MGEs
  - Higher prevalence of SEG (61) to SEA (24) suggests that the isolates don't contain Sa3

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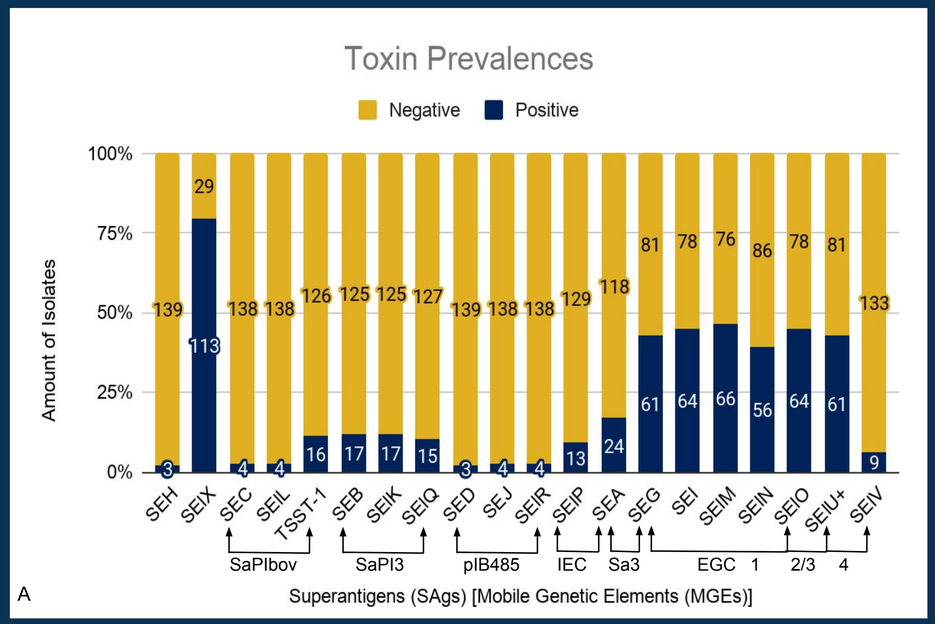
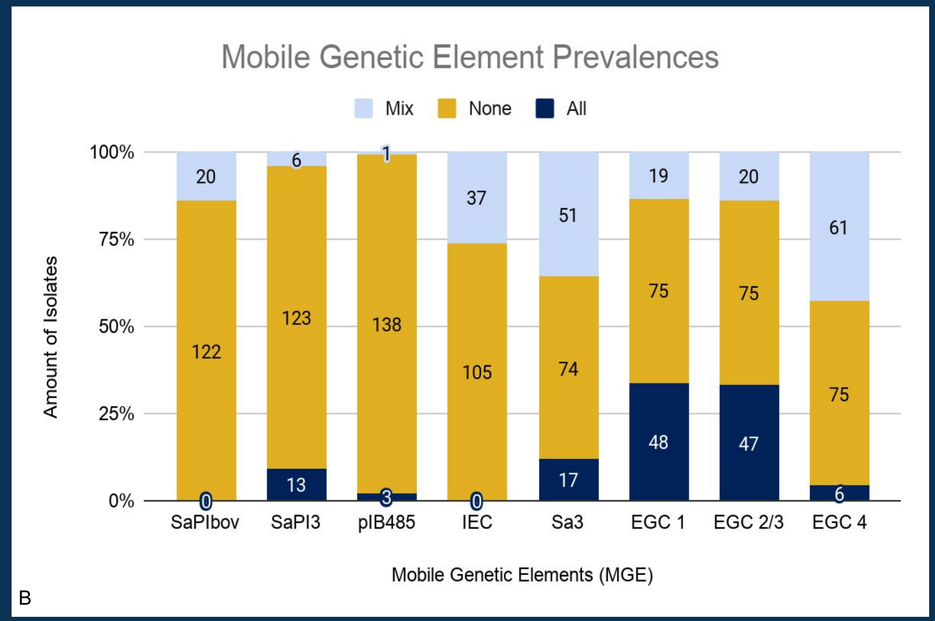
The enterotoxin gene clusterings and other mobile genetic elements affect the superantigen prevalences



A



B

Additional Superantigen Information

- Staphylococcal Enterotoxins (SEs)
  - Category B select agents
  - Resistant to heat and acid
  - Express emetic activity
    - Throwing up
  - Staphylococcal Enterotoxin-like (SEI)
    - SEs that lack or haven't been tested for emetic activity
    - Designation to infer their role in staphylococcal food poisoning isn't confirmed
- In-depth look at a couple of the SAgs:
  - Staphylococcal Enterotoxin A (SEA)
    - Most common in staph related food poisoning
  - Toxic Shock Syndrome Toxin-1 (TSST-1)
    - Cause of menstrual TSS and half of non-menstrual TSS
    - Has the ability to cross mucosal barriers

Additional MGE Information

- Mobile genetic elements are methods of transferring DNA encoding virulence factors, resistance determinants and enzymes that assist with the transfer and integration into host
- MGEs are seen in the forms of plasmids, transposons, insertion sequences, bacteriophages, pathogenicity islands and genomic islands
- Enterotoxin Gene Clustering (EGC)
  - Found on the chromosomal operon
  - EGC 1 = SEG, SEI, SEIM, SEIN and SEIO
  - EGC 2/3 = SEG, SEI, SEIM, SEIN, SEIO and SEIU
  - EGC 4 = SEG, SEI, SEIM, SEIN, SEIO, SEIU and SEIV
- Staphylococcal Pathogenicity Islands (SaPI)
  - Found on chromosomes and travel through bacteriophages
  - SaPIbov = SEC, SEIL and TSST-1
  - SaPI3 = SEB, SEIK and SEIQ
- Plasmids
  - pIB485 = SED, SEJ and SEIR
- Immune Evasion Cluster (IEC)
  - IEC = SEA (Variants A and D) and SEIP (Variants F and G)
  - IEC also contains SCN, SAK and CHP
  - Present in bacteriophages
- Bacteriophages
  - Greatest impact on diversity due to allowing other MGEs to be mobile through them
  - phage Sa3 = SEA and SEG
- Superantigens
  - Can be found on one to multiple different MGEs
    - Example: SEB can be found on certain SaPIs and plasmids

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